Amendments to the Specification

Please replace the paragraph starting on page 5, line 25 with the following paragraph:

Examples for peptide candidates with potential immunogenicity that can be derived from the tumor-associated antigen of the present invention, are the CAMEL-derived peptides with the sequence HLSPDQGRF (SEQ ID NO: 29) and LMAQEALAF (SEQ ID NO: 30) for HLA-A3 or RMAVPLLRR (SEQ ID NO: 31) for HLA-A3101. Similarly, other peptides for these or for other alleles can be determined by the method mentioned above.

Please replace the paragraph starting on page 10, line 24 with the following paragraph:

NY-ESO-1 also has been described as the target of melanoma-specific HLA-A*0201 restricted CTL clones, which recognize an epitope translated in ORF3, located between aa 155 and 167 (Jäger et al., 1998). Therefore, it is very likely that also LAGE-1^S will be recognized by these clones, but not LAGE-1^L, since the protein sequence is different at this part of the molecule. The CAMEL-specific CTL clones recognize a peptide in an alternative reading frame, which is encoded in both LAGE-1 and NY-ESO-1. This means that tumor cells expressing either LAGE-1 or NY-ESO-1 can be recognized by MLMAQEALAFL (SEQ ID NO: 11) -specific CTL, which might enlarge the number of tumors that can be treated with immunotherapy based on this peptide.

Please replace the paragraph starting on page 12, line 3 with the following paragraph:

b) The effects of increasing concentrations of peptides, derived from the major target epitope MLMAQEALAFL (SEQ ID NO: 11) on recognition by CTL 1/29. Various concentrations of peptides as indicated were loaded on HLA-A*0201+ cells and tested in a TNF-α release assay with CTL 1/29.

Please replace the paragraph starting on page 20, line 9 with the following paragraph:

At a peptide concentration of 10 μg/ml only the N-terminal 11- and 10-mer peptides (M)LMAQEALAFL (SEQ ID NO: 11 and NO: 12) induced preponderant recognition by CTL 1/29 (Fig. 3a), indicating that the epitope recognized by the CTL is located in the first 11 amino acids of the CAMEL-encoded protein. Closer inspection of peptides derived of this N-terminal 11-mer in a peptide concentration dependent TNF-α release assay (Fig. 3b) revealed that the methionine at position 1 as well as the leucine at position 11 are of crucial importance for reconstituting CTL reactivity. Deletion of either of these amino acids leads to an at least 5 decades higher peptide concentration required for comparable TNF-α release. The only other peptide showing weak activity is the 3-11 MAQEALAFL (SEQ ID NO:33). In contrast, the MLMAQEALA (SEQ ID NO: 34) has no activity at all (Fig. 3b), suggesting that the C-terminal amino acids FL do significantly contribute to the recognition by the CTL.

Please replace the paragraph starting on page 21, line 14 with the following paragraph:

It was examined whether cells transfected with the complete LAGE-1 (or NY-ESO-1) cDNA clones are able to stimulate CTL 1/29. Remarkably, COS/HLA-A*0201 cells transfected with LAGE-1^S, the alternatively spliced LAGE-1^L (as well as with the NY-ESO-1) cDNA are able to stimulate CTL 1/29 (Fig. 4). This indicates that, at least in COS-7 cells, protein translation also starts from the second start codon at nucleotide 94 in LAGE-1^S, notwithstanding the presence of the first ATG at position 54. Also in this case, this results in the "alternative reading frame" peptide, MLMAQEALAFL (SEQ ID NO: 11), recognized by CTL 1/29.

Please insert the Substitute Sequence Listing submitted herewith at the end of the application in place of the previously submitted sequence listing.